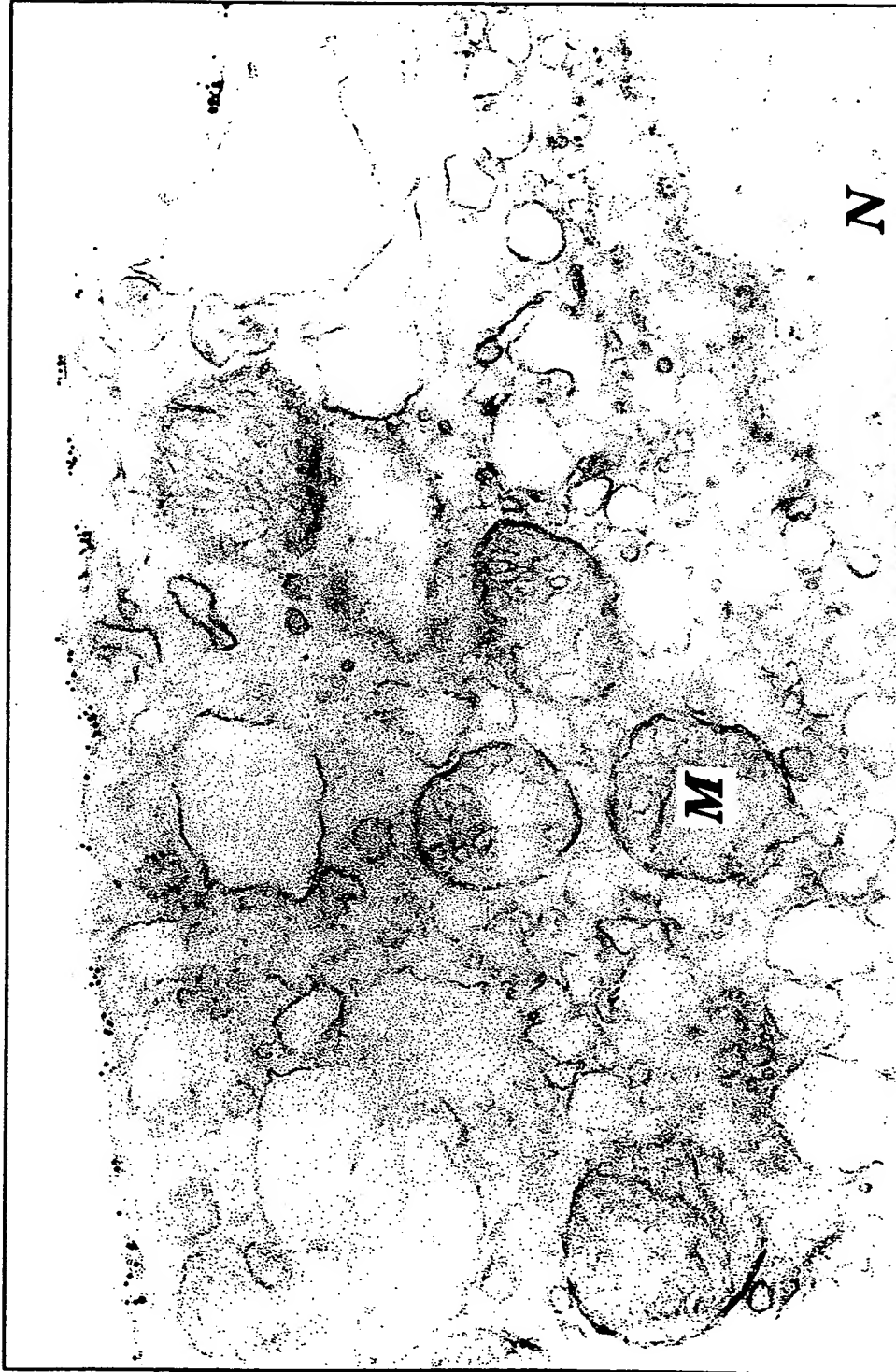


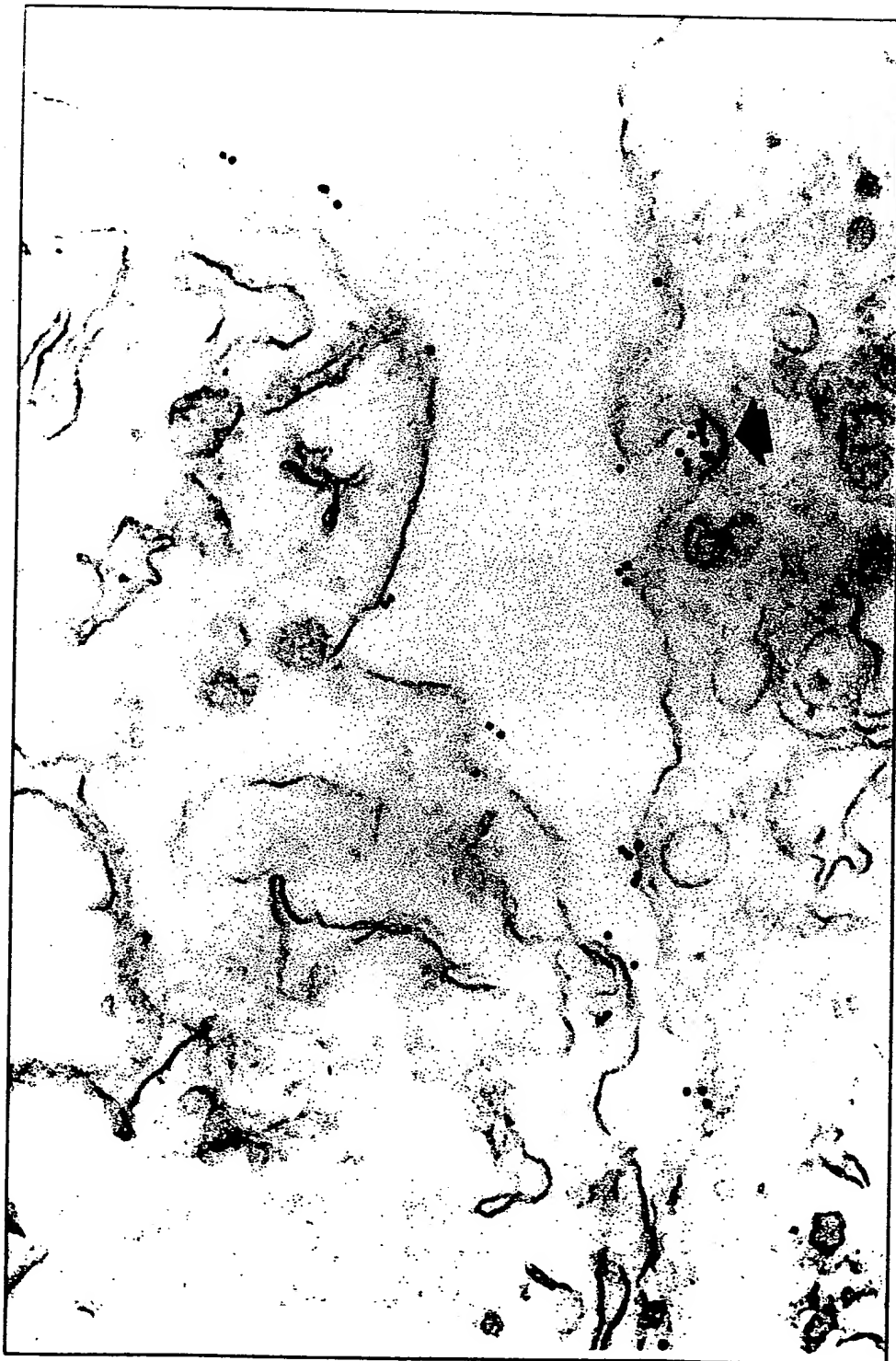
01/12



**FIG. 1**

FOOT-510000

02/12



**FIG. 2**

FILE: 51502000

03/12



**FIG. 3**

FIG. 3

04/12



**FIG. 4**

FIG. 4 - 5130000

05/12



**FIG. 5**

FIG. 5

06/12

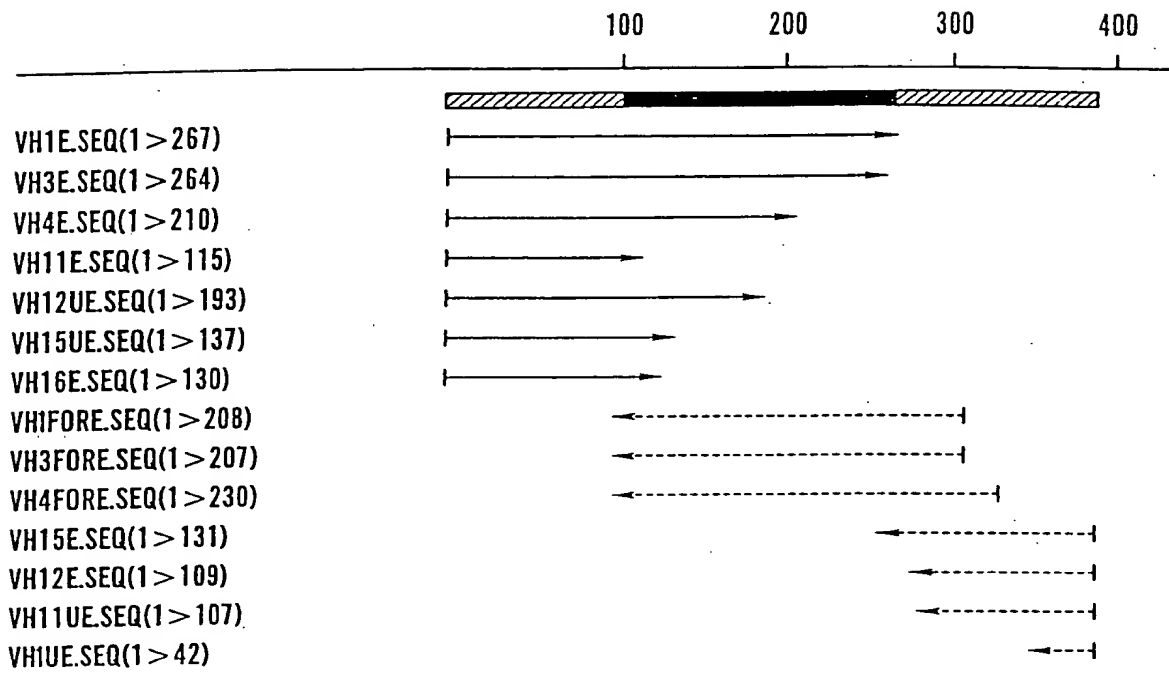


FIG. 6

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE



08/12

LIPMAN-PEARSON PROTEIN ALIGNMENT  
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGTSVRLSCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT  
 EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:  
 EVQLQQSGPELVKPGASVKISCKASGYTFITDYMINWVKQSPGKSLEWIGDINPGNGGTS  
 YNQKFEDKATLIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGGIT  
 YNQKF.:KATLIVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGGGIT  
 YNQKFKGKATLIVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSYMAYYAFDYWGQGIT

10 20 30 40 50  
 60 70 80 90 100 110  
 120

LTVSS  
 :TVSS  
 VIVSS

FIG. 8



09/12

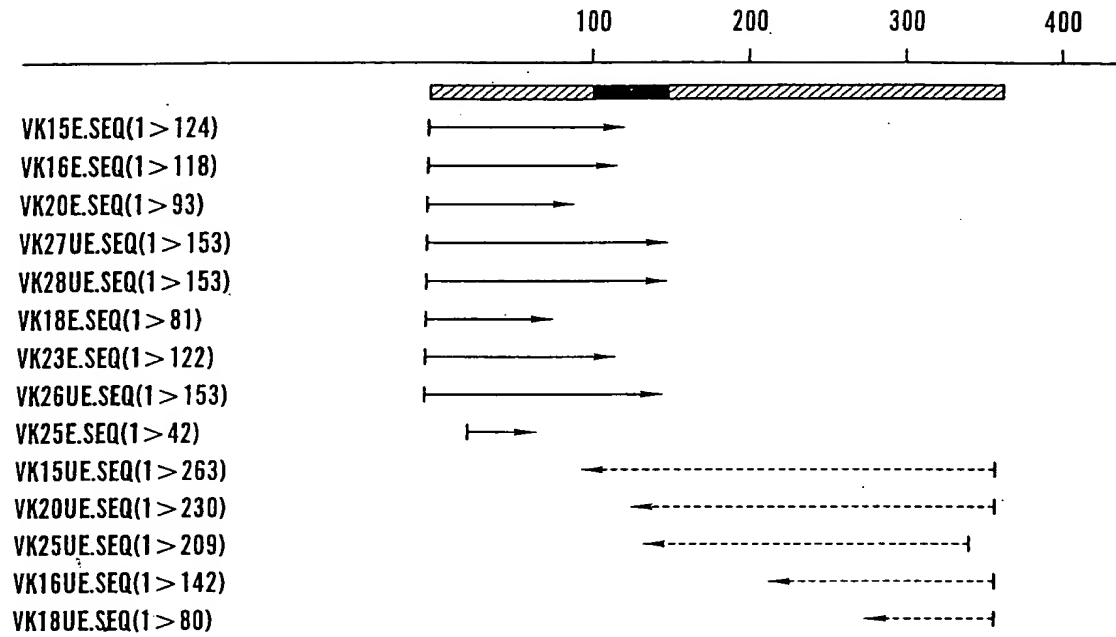


FIG. 9

10/12

ENZYMES: ALL 74 ENZYMES (NO FILTER):  
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

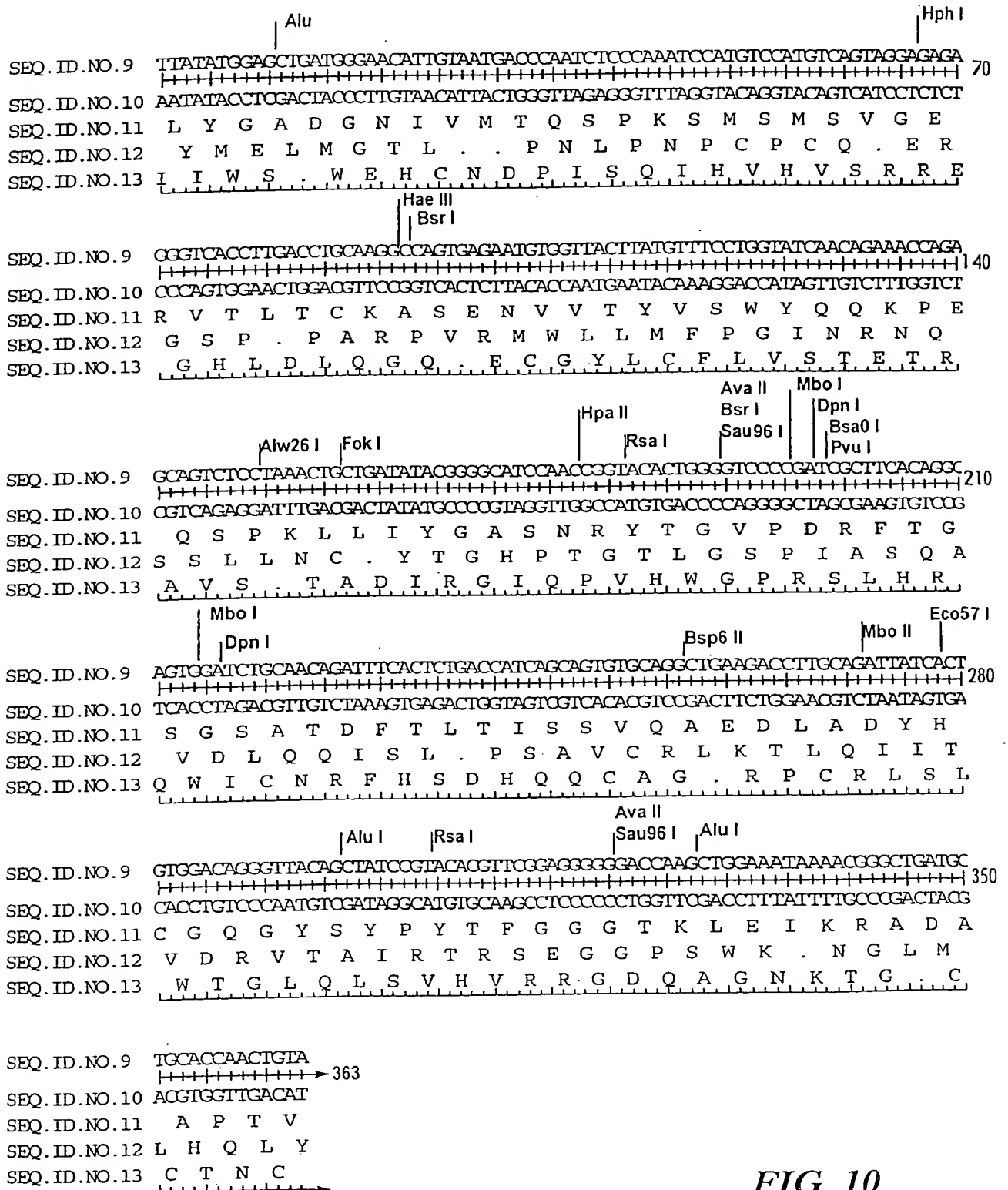


FIG. 10

11/12

LIPMAN-PEARSON PROTEIN ALIGNMENT  
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10      ↓20      ↓30      ↓40      ↓50  
NIVMTIQSPKSMMSVGERVILTICKAS-ENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVP  
:I MTQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQKP. SPKLLIY AS. ..GVP  
DIQMTIQSPSSLSASLGDRVTITCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP  
↑10      ↑20      ↑30      ↑40      ↑50      ↑60  
↓60      ↓70      ↓80      ↓90      ↓100  
DRFTGSGSATDFILTISSVQAEDLADYHCGQGYSY-PYTFGGGKLEIK  
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK  
SRFSGSGSGTDYSLTISNLEQEDLATYFQQQNTLPPRTFGGGKLEIK  
↑70      ↑80      ↑90      ↑100

FIG. 11

12/12

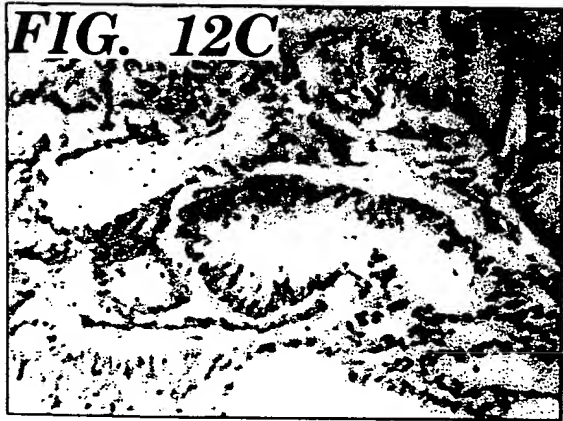


FIG. 12A